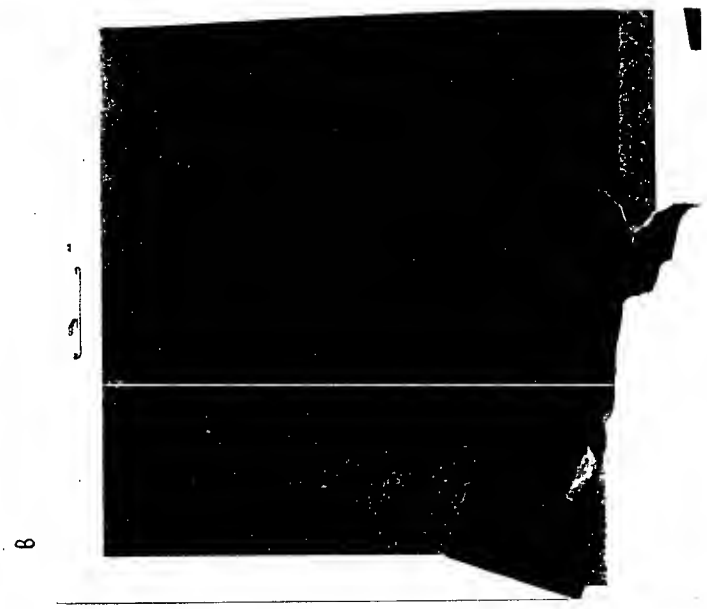

Fig 1b

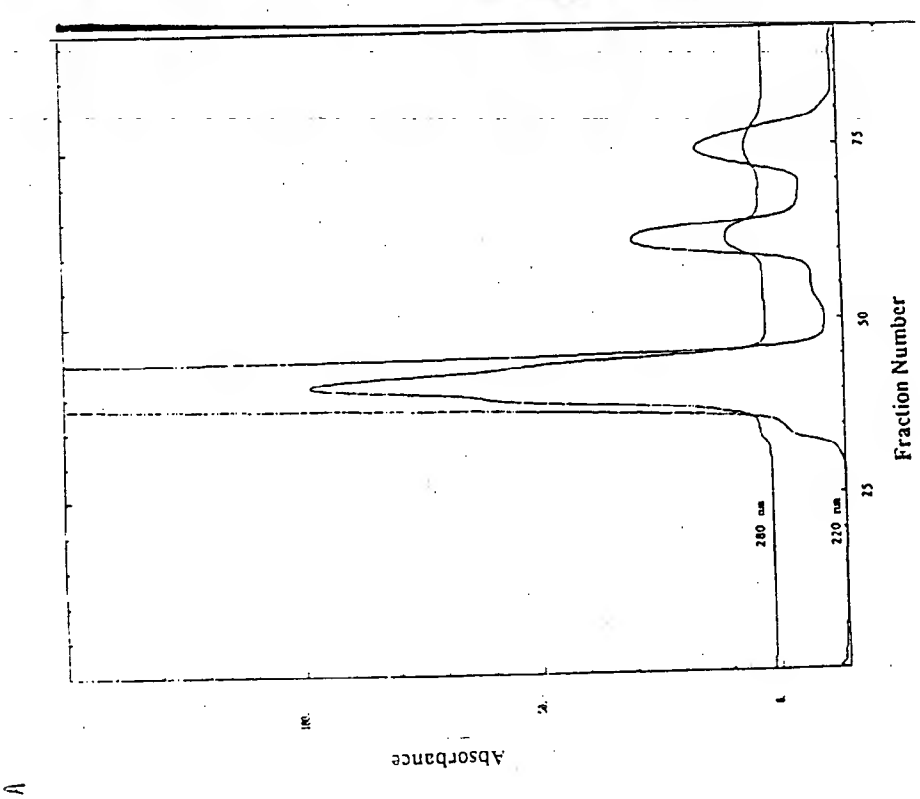

Fig 1a

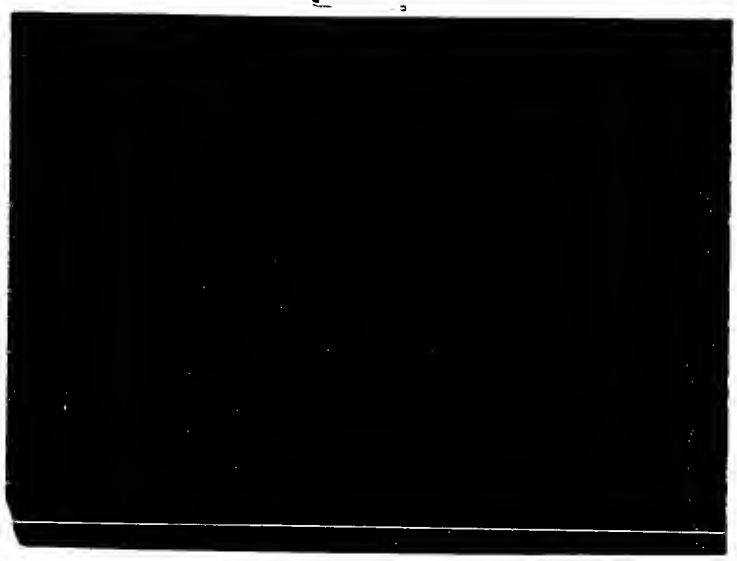

Fig. 2

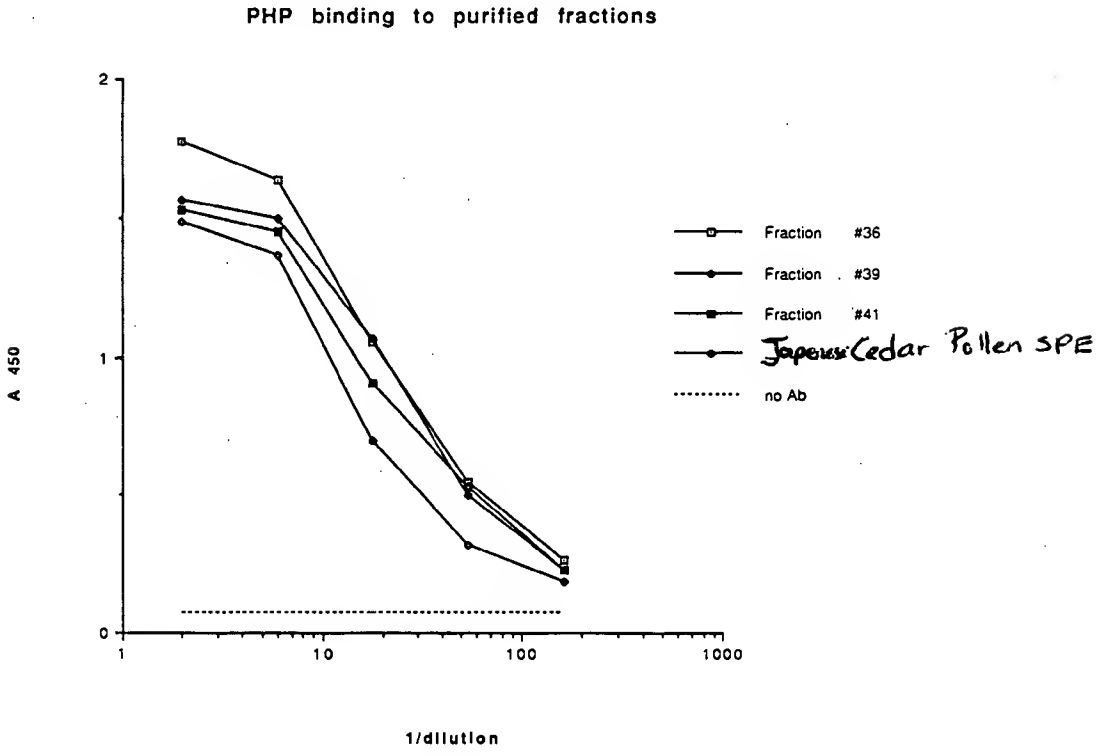

Fig. 3

Fig. 4a


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5'-AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC      60

AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT             107
      Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
      -21 -20                 -15                 -10

GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA           155
Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
        -5                   1                   5

GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA           203
Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
 10                  15                  20                  25

GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT           251
Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
                30                  35                  40

ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT           299
Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
            45                  50                  55

CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT           347
Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
        60                  65                  70

GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT           395
Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr
    75                  80                  85

AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT           443
Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly
 90                  95                 100                 105

CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG           491
Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu
                110                 115                 120

TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC           539
Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn
            125                 130                 135

GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT           587
Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu
        140                 145                 150

ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC           635
Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
    155                 160                 165
```

Fig. 4b

```
AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT                683
Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val
170                 175                 180                 185

ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA               731
Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu
                190                 195                 200

GGG CAT GAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG               779
Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val
            205                 210                 215

GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA               827
Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala
        220                 225                 230

CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT               875
Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr
    235                 240                 245

ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG               923
Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly
250                 255                 260                 265

AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG AAG CAA GTA ACC ATA               971
Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile
                270                 275                 280

CGT ATT GGA TGC AAA ACA TCA TCA TCT TGT TCA AAT TGG GTG TGG CAA              1019
Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln
            285                 290                 295

TCT ACA CAA GAT GTT TTT TAT AAT GGA GCT TAT TTT GTA TCA TCA GGG              1067
Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly
        300                 305                 310

AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT              1115
Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val
    315                 320                 325

GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA              1163
Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu
330                 335                 340                 345

ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC             1217
Thr Cys Ser Leu Ser Lys Arg Cys
                350

TATCTAAATT AACATCAACA AGAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA            1277

AATAAAAATG TATCTTTTAC TATTAAAAAA AAAAATGATC GATCGGACGG TACCTCTAGA-3'        1337
```

Japan Cedar Pollen SPE

Fig 5a 1/938990

A

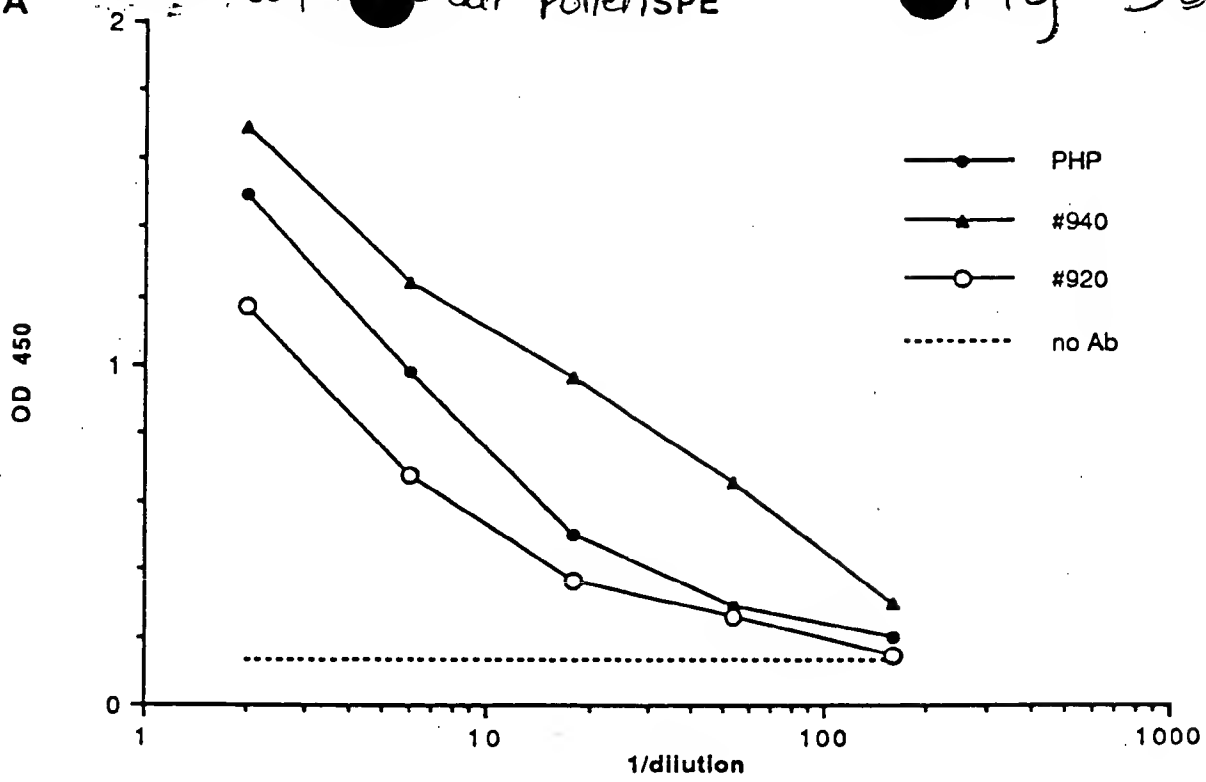
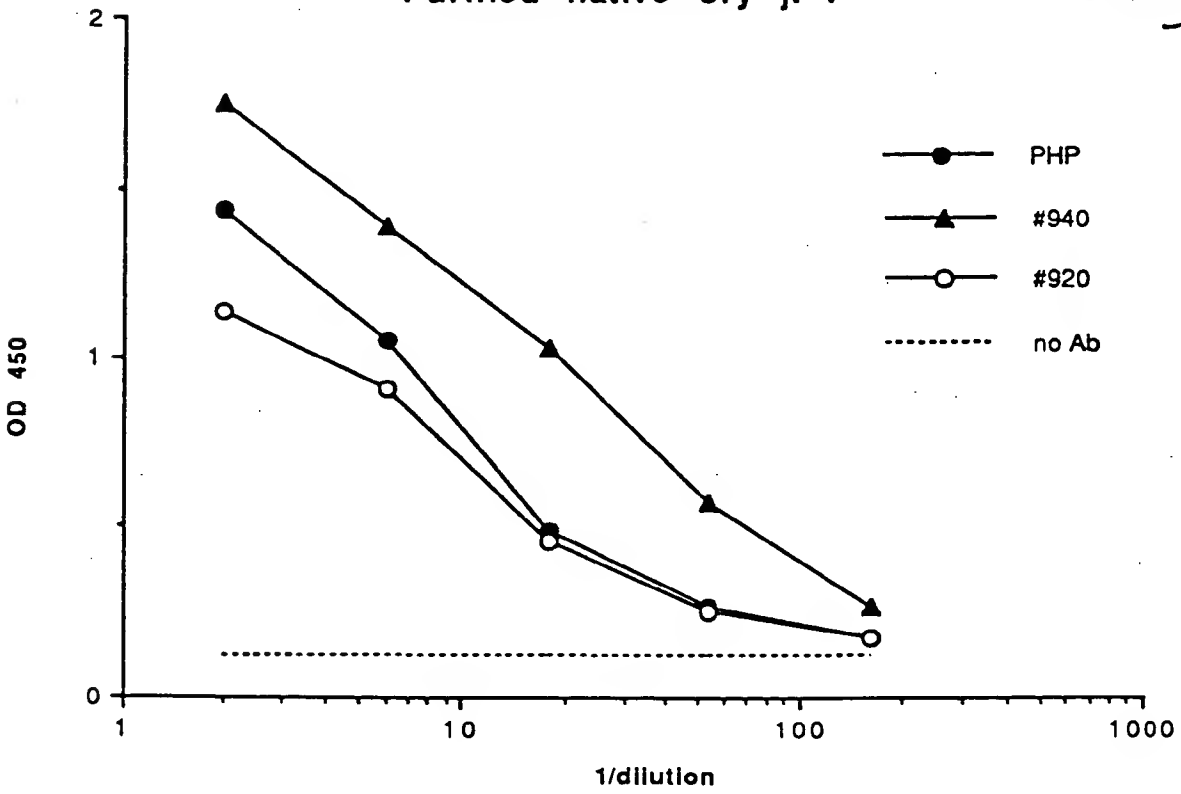


Fig. 5b

B

Purified native Cry j. I



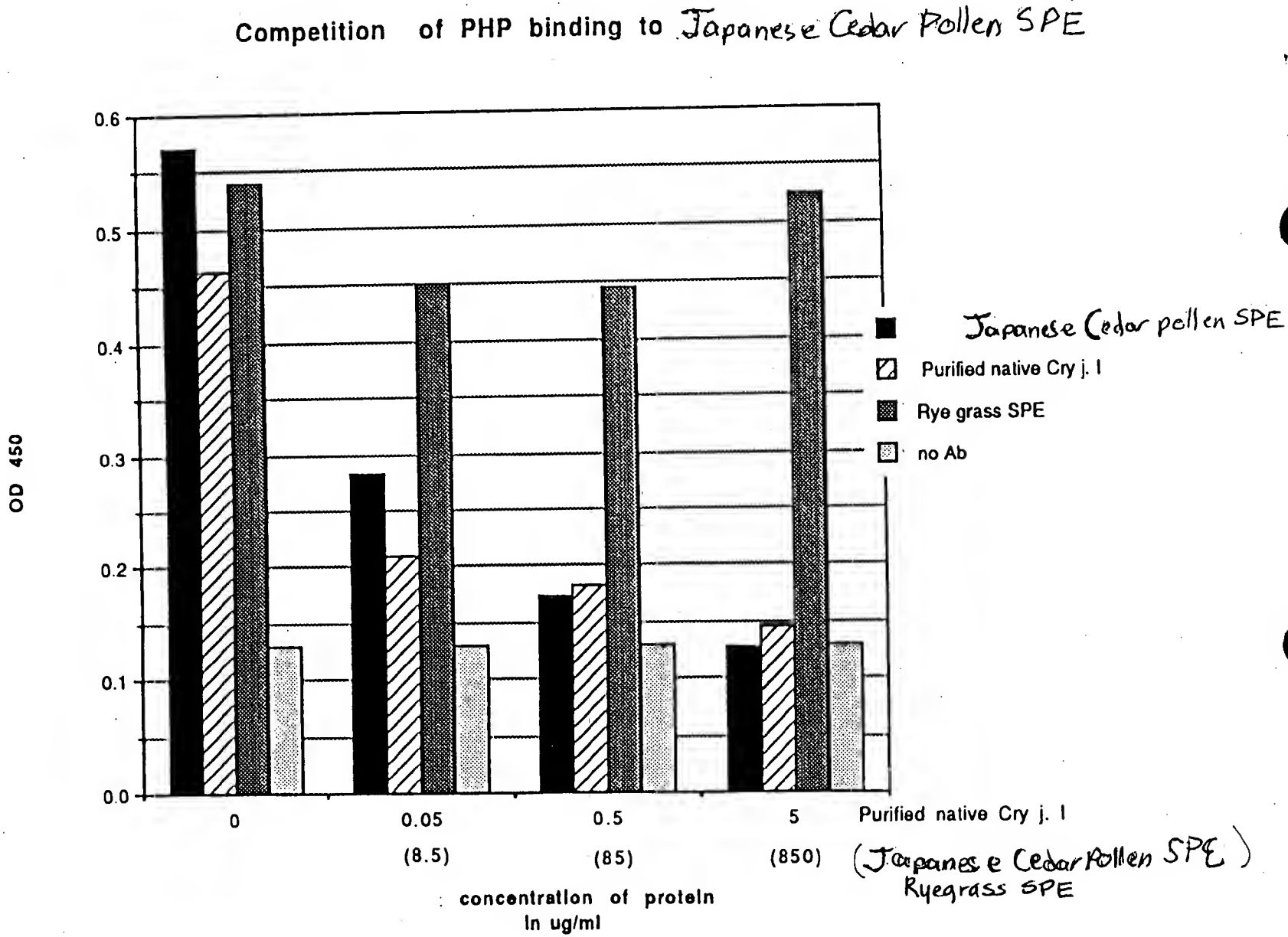


Fig. 6

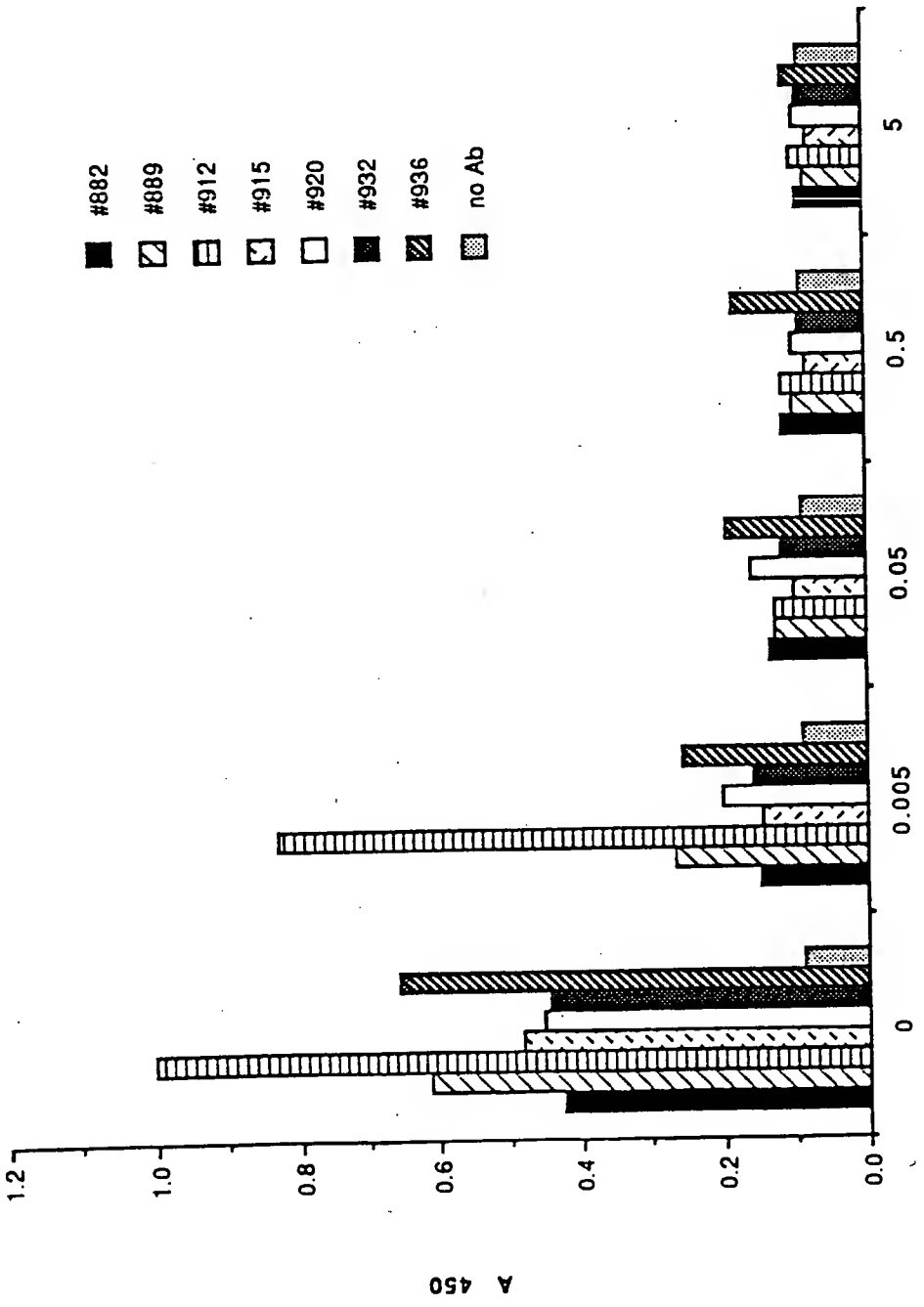
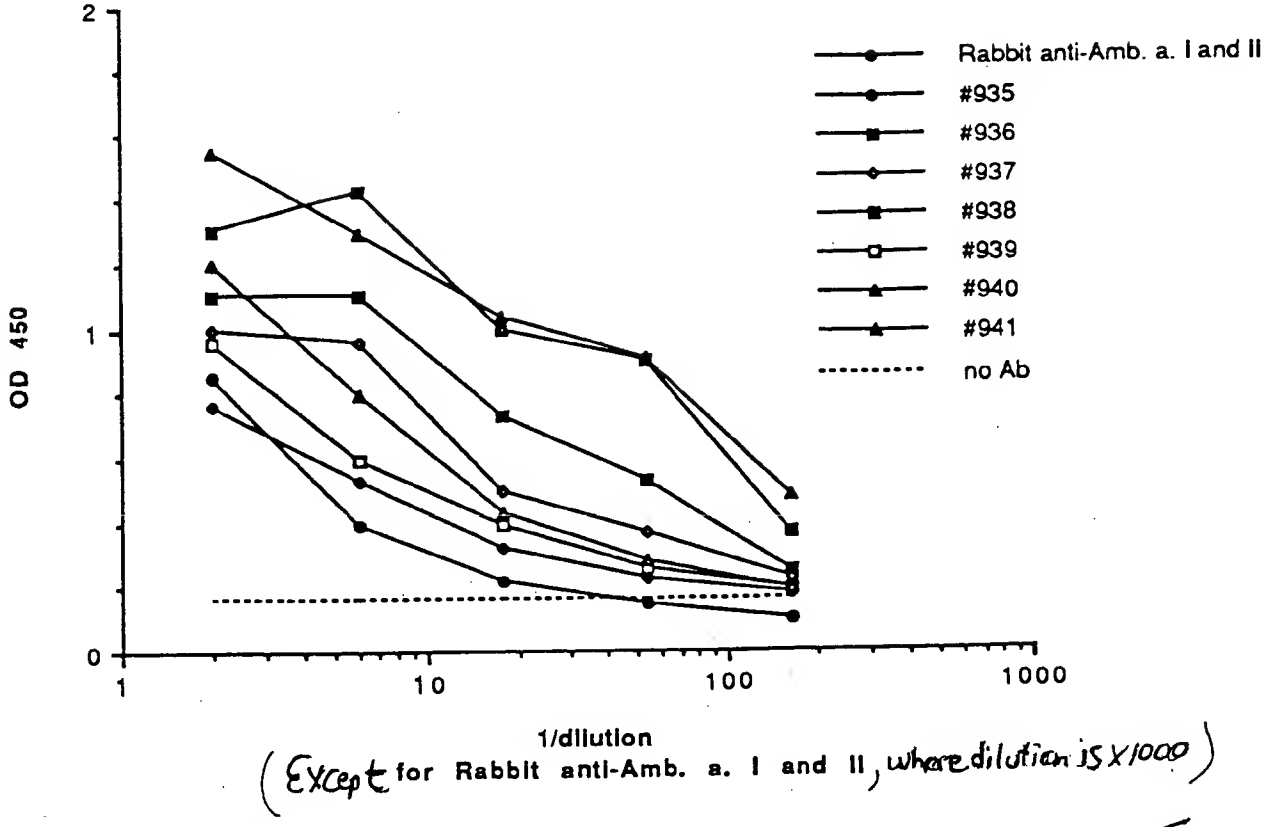


Fig. 7

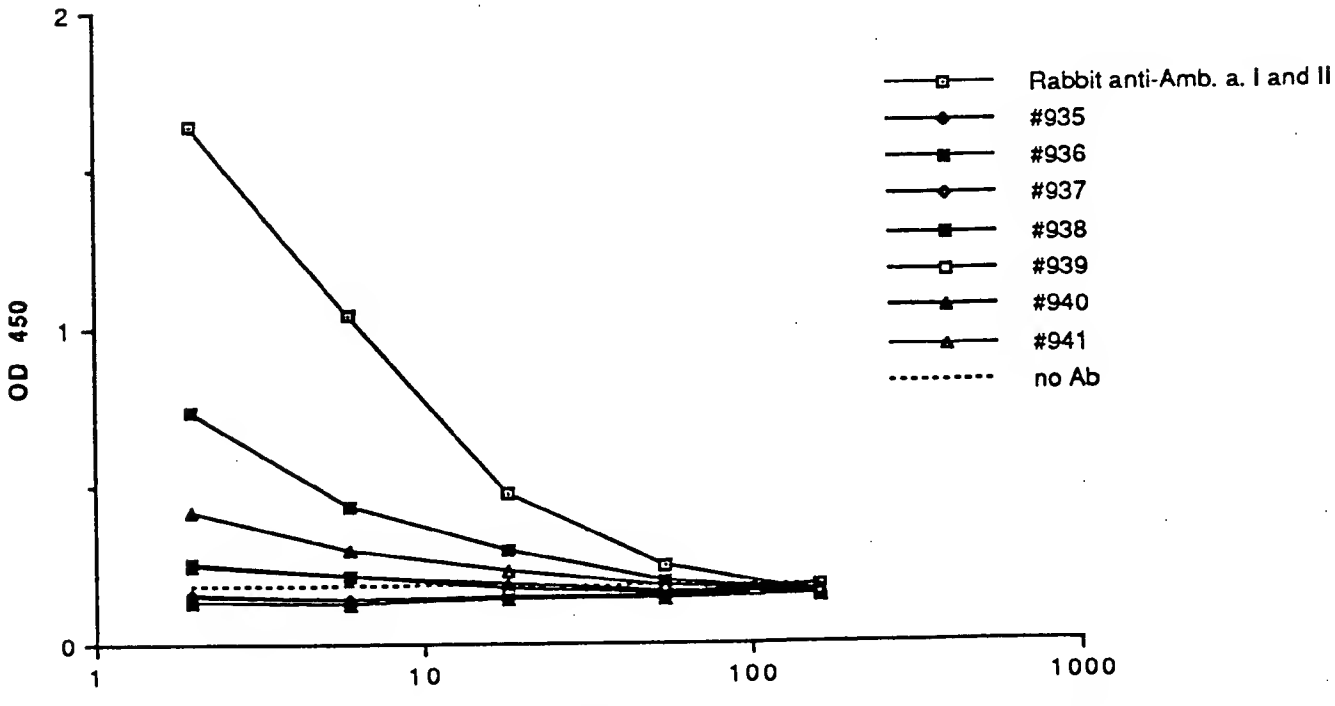
A



(Except for Rabbit anti-Amb. a. I and II, where dilution is X1000)

B

Fig. 8b



Except for Rabbit anti-Amb. a. I and II, where dilution is X1000)

8/15

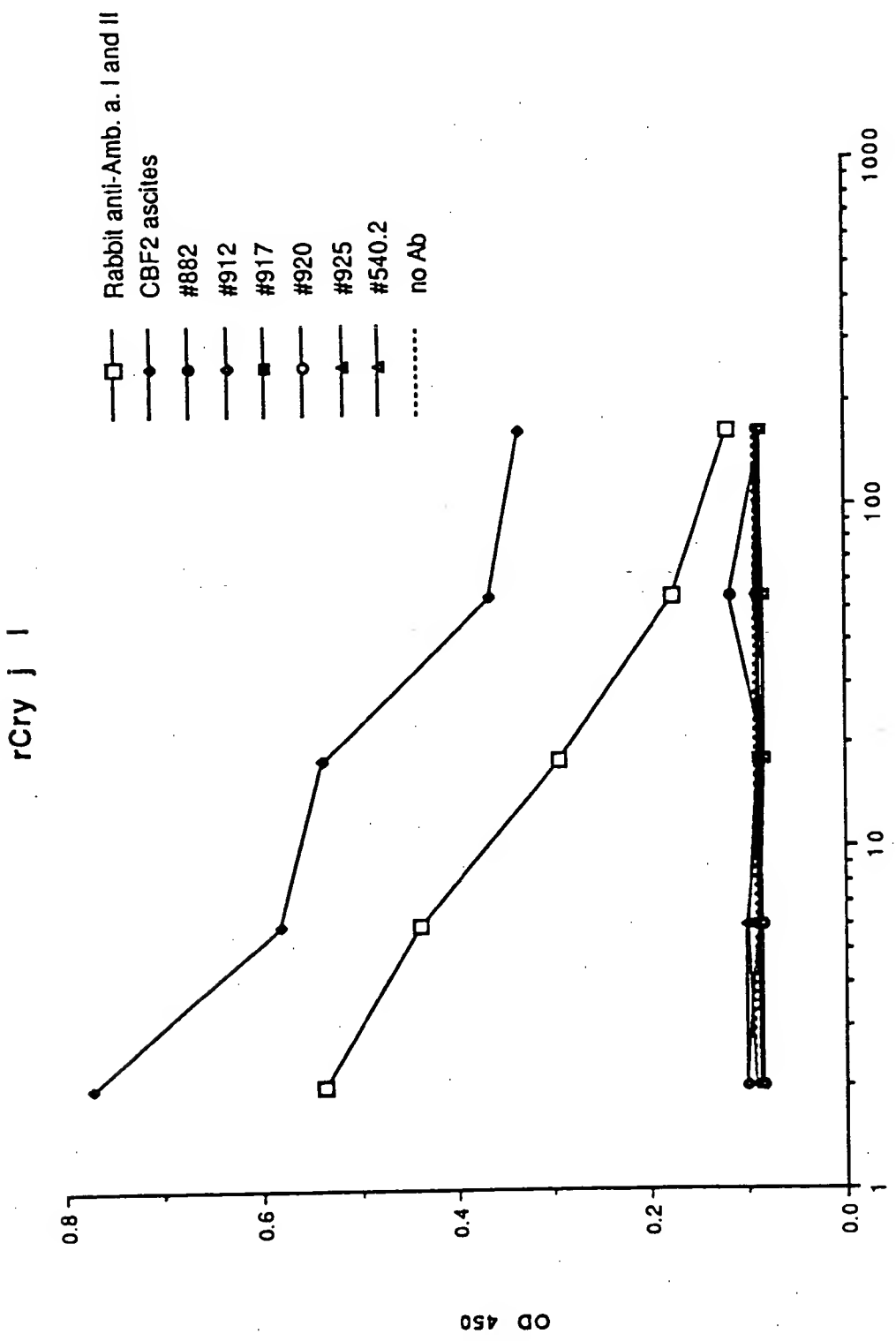
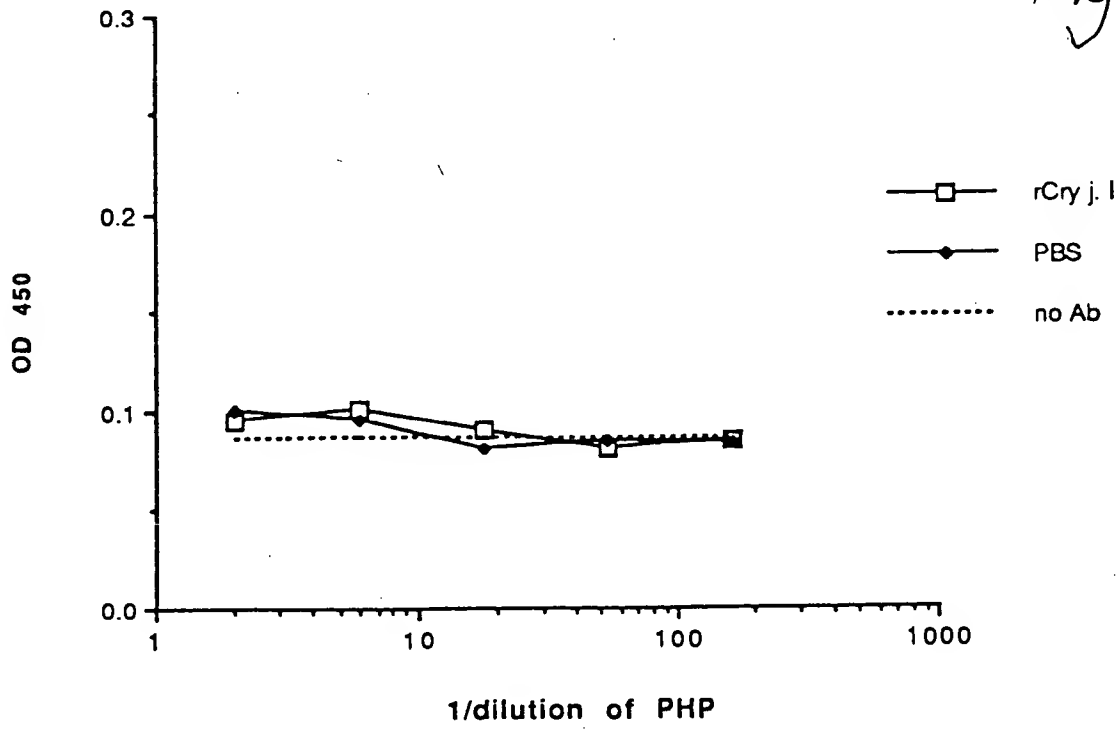


Fig. 9

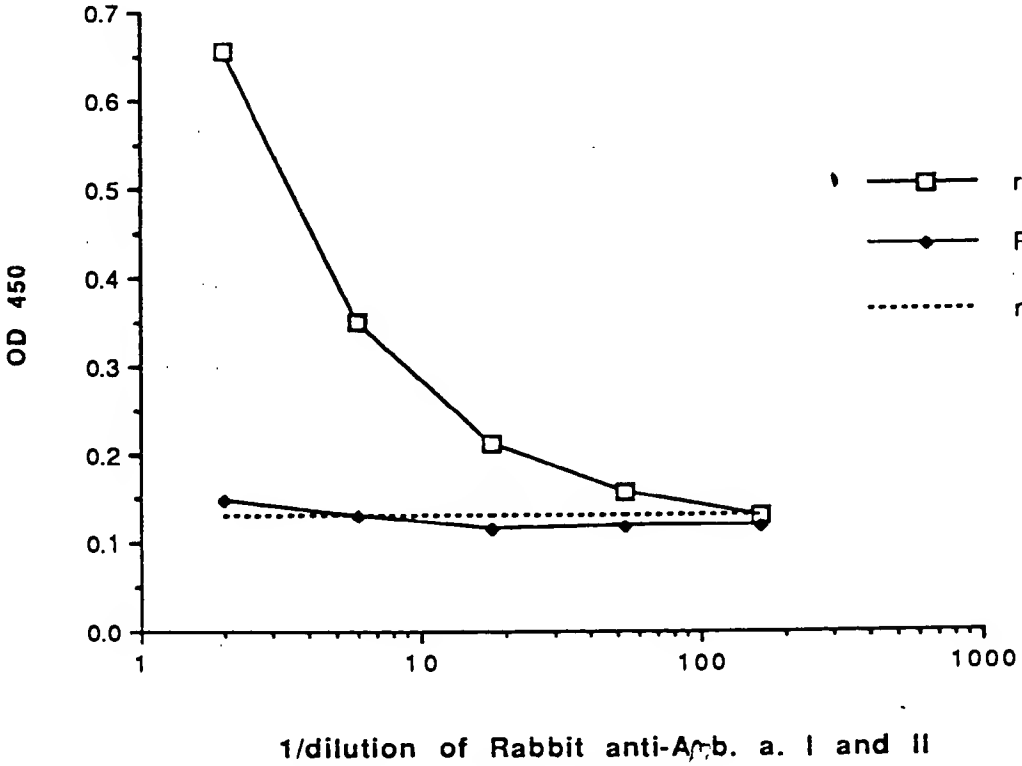
A Capt[redacted] ELISA with CBF2 (IgG) m[redacted]

Fig. 10a



B Capture ELISA with CBF2 (IgG) mAb

Fig. 10b



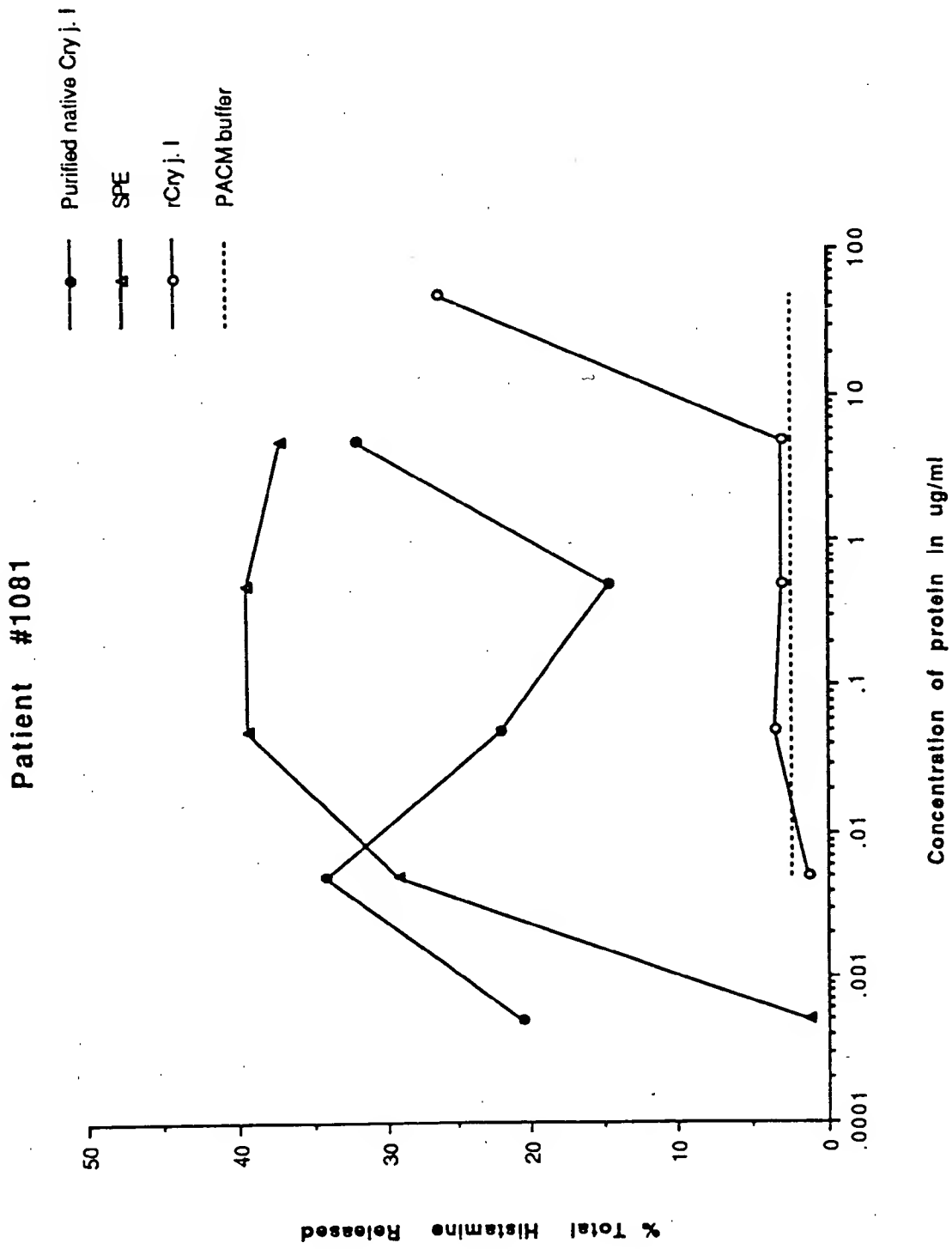
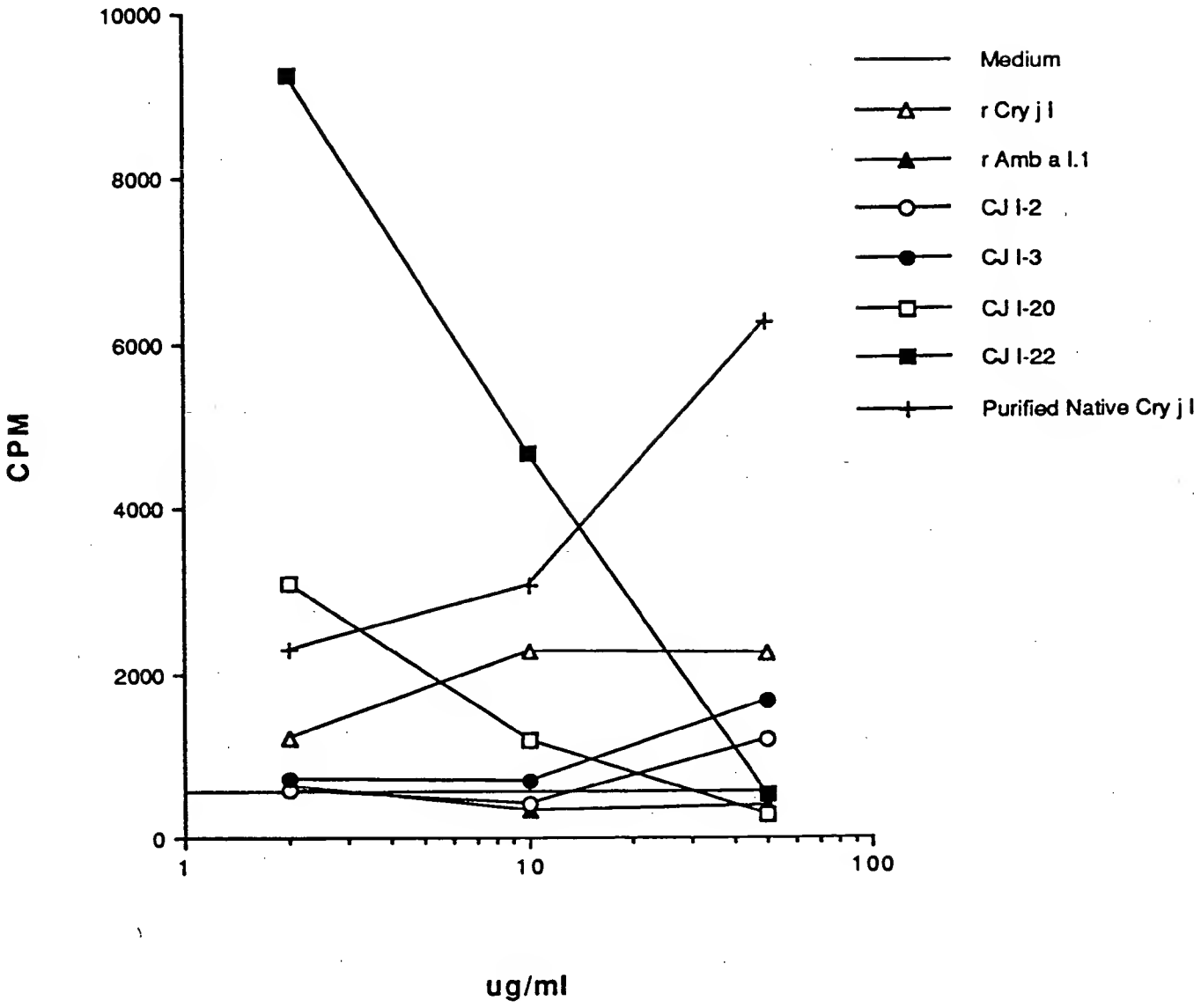


Fig - 11

Fig. 12



Peptide Name	
CJI-1 (1-20)	D N P I D S C W R G D S N W A Q N R M K
CJI-2 (11-30)	D S N W A Q N R M K L A D C A V G F G S
CJI-3 (21-40)	L A D C A V G F G S S T M G G K G G D L
CJI-4 (31-50)	S T M G G K G G D L Y T V T N S D D D P
CJI-5 (41-60)	Y T V T N S D D D P V N P A P G T L R Y
CJI-6 (51-70	V N P A P G T L R Y G A T R D R P L W I
CJI-7 (61-80)	G A T R D R P L W I I F S G N M N I K L
CJI-8 (71-90)	I F S G N M N I K L K M P M Y I A G Y K
CJI-9 (81-100)	K M P M Y I A G Y K T F D G R G A Q V Y
CJI-10 (91-110)	T F D G R G A Q V Y I G N G G P C V F I
CJI-11 (101-120)	I G N G G P C V F I K R V S N V I I H G
CJI-12 (111-130)	K R V S N V I I H G L Y L Y G C S T S V
CJI-13 (121-140)	L Y L Y G C S T S V L G N V L I N E S F
CJI-14 (131-150)	L G N V L I N E S F G V E P V H P Q D G
CJI-15 (141-160)	G V E P V H P Q D G D A L T L R T A T N
CJI-16 (151-170)	D A L T L R T A T N I W I D H N S F S N
CJI-17 (161-180)	I W I D H N S F S N S S D G L V D V T L
CJI-18 (171-190)	S S D G L V D V T L T S T G V T I S N N
CJI-19 (181-200)	T S T G V T I S N N L F F N H H K V M L
CJI-20 (191-210)	L F F N H H K V M L L G H D D A Y S D D
CJI-21 (201-220)	L G H D D A Y S D D K S M K V T V A F N
CJI-22 (211-230)	K S M K V T V A F N Q F G P N C G Q R M
CJI-23 (221-240)	Q F G P N C G Q R M P R A R Y G L V H V
CJI-24 (231-250)	P R A R Y G L V H V A N N N Y D P W T I
CJI-25 (241-260)	A N N N Y D P W T I Y A I G G S S N P T
CJI-26 (251-270)	Y A I G G S S N P T I L S E G N S F T A
CJI-27 (261-280)	I L S E G N S F T A P N E S Y K K Q V T
CJI-28 (271-290)	P N E S Y K K Q V T I R I G C K T S S S
CJI-29 (281-300)	I R I G C K T S S S C S N W V W Q S T Q
CJI-30 (291-310)	C S N W V W Q S T Q D V F Y N G A Y F V
CJI-31 (301-320)	D V F Y N G A Y F V S S G K Y E G G N I
CJI-32 (311-330)	S S G K Y E G G N I Y T K K E A F N V E
CJI-33 (321-340)	Y T K K E A F N V E N G N A T P Q L T K
CJI-34 (331-350)	N G N A T P Q L T K N A G V L T C S L S
CJI-35 (341-353)	N A G V L T C S L S K R C

Fig. 13

Fig. 14

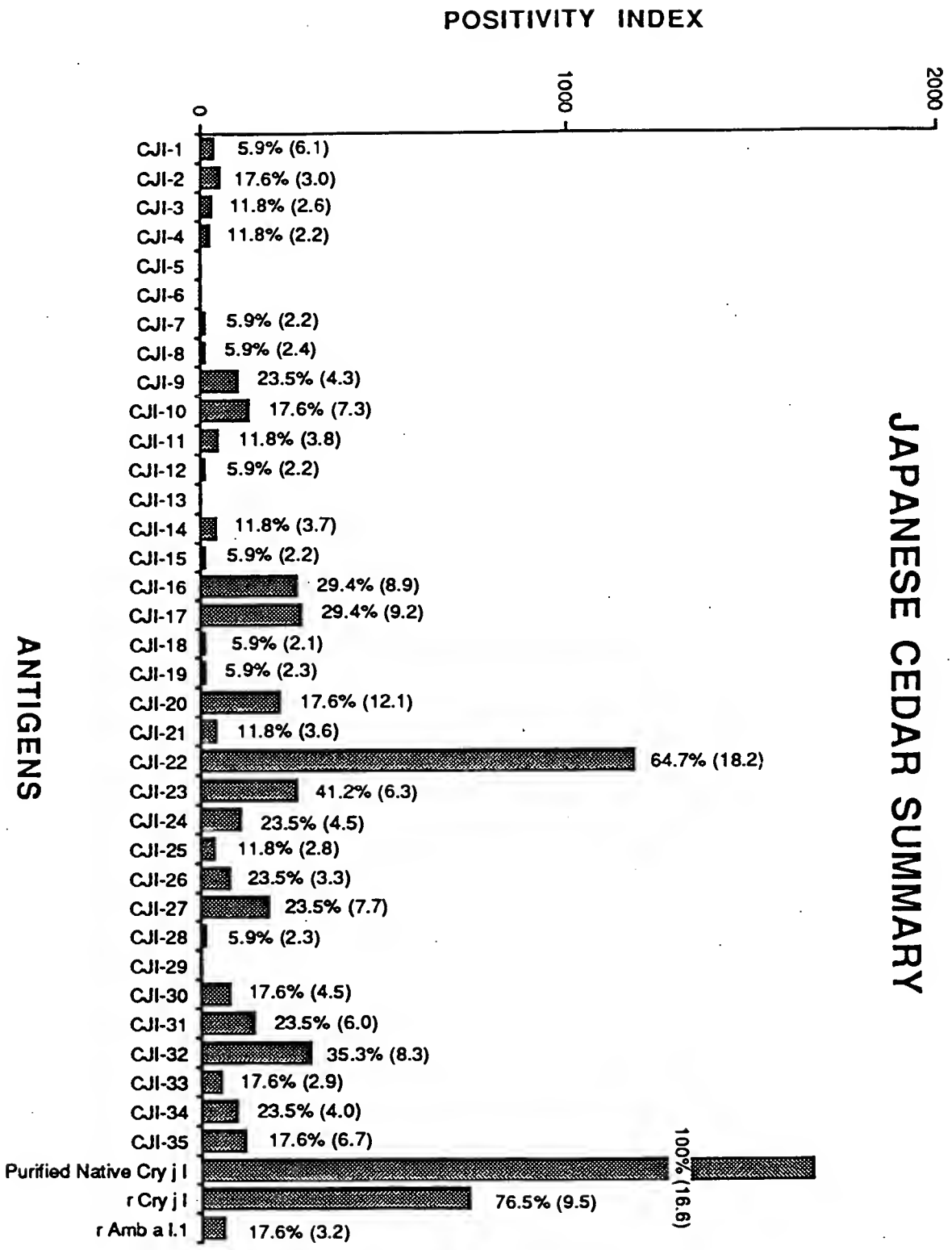


Fig. 15a

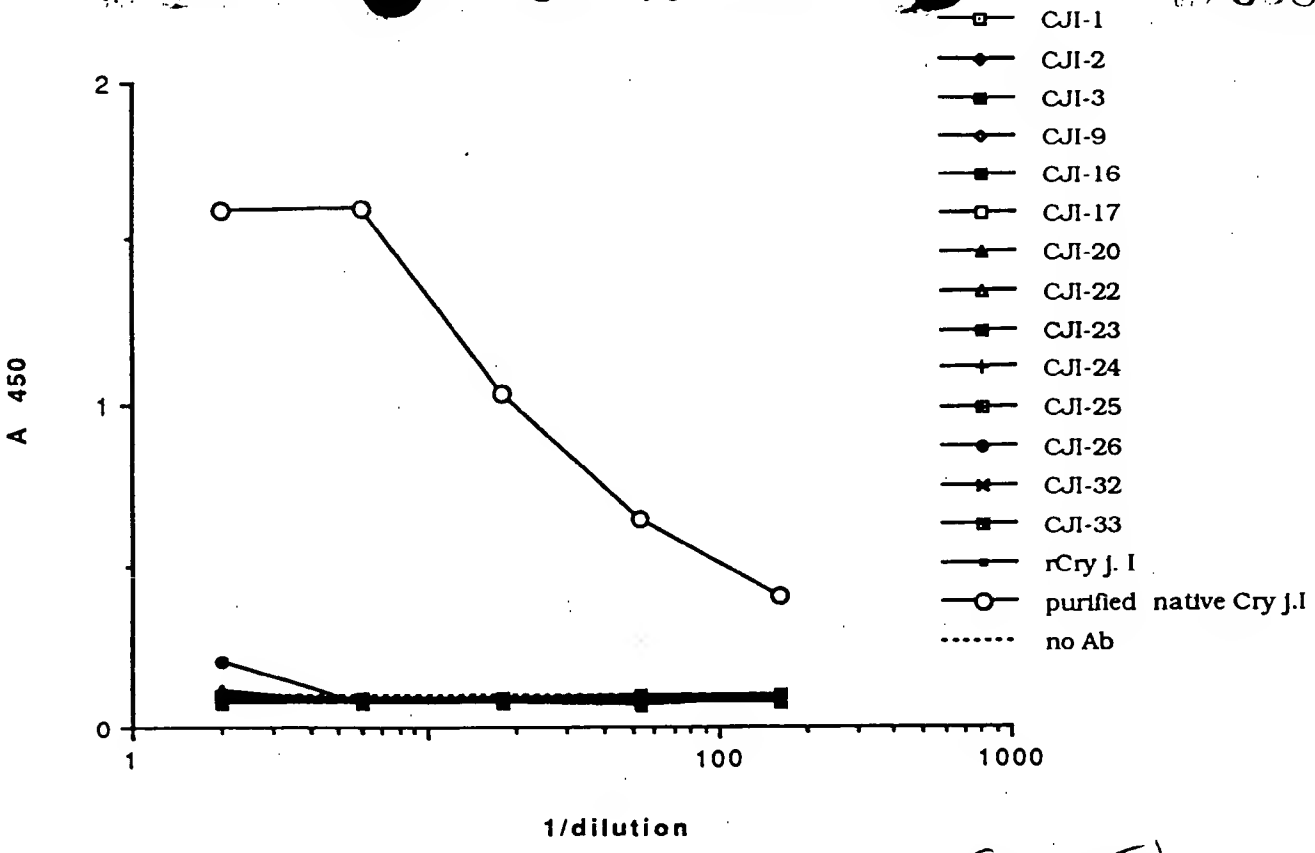


Fig. 15b